AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows.

Specification

Page 4, Lines 4 - 17

According to the present invention, there is further provided a method for determining an inflammatory disease, which comprises detecting at least one single nucleotide polymorphism selected from the group consisting of the following (1) to (5):

(1) a G/A polymorphism at nucleotide 10 in the nucleotide sequence of exon 1 of the LT-α gene shown in SEQ ID NO: 1;

(2) an A/G polymorphism at nucleotide 90 in the nucleotide sequence of intron 1 of the LT-α gene shown in SEQ ID NO: 2;

(3) a C/A polymorphism at nucleotide ~~81~~ 80 in the nucleotide sequence of exon 3 of the LT-α gene shown in SEQ ID NO: 3;

(4) a T/A polymorphism at nucleotide 572 in the nucleotide sequence of a promoter of the IKBL gene shown in SEQ ID NO: 4; and

(5) a G/C polymorphism at nucleotide 1228 in the nucleotide sequence of a promoter of the BAT1 gene shown in SEQ ID NO: 5.

Page 4, lines 24 - 29; Page 5, lines 1 – 10

According to the present invention, there is further provided an oligonucleotide that can hybridize to a sequence of at least 10 continuous nucleotides containing at least one position selected from the group consisting of the following (1) to (5), the position being contained in the sequences shown in SEQ ID NOS: 1 to 5, or to a complementary sequence thereof, and is used as a probe in the above determination method:

(1) position 10 of the nucleotide sequence of exon 1 of the LT-α gene shown in SEQ ID NO: 1;

(2) position 90 of the nucleotide sequence of intron 1 of the LT-α gene shown in SEQ ID NO: 2;

(3) position ~~81~~ 80 of the nucleotide sequence of exon 3 of the LT-α gene shown in SEQ ID NO: 3;

(4) position 572 of the nucleotide sequence of the promoter of the IKBL gene shown in SEQ ID NO: 4; and

(5) position 1228 of the nucleotide sequence of the promoter of the BAT1 gene shown in SEQ ID NO: 5.

Page 5, lines 11 – 26

According to the present invention, there is further provided an oligonucleotide that can amplify a sequence of at least 10 continuous nucleotides containing at least one position selected from the group consisting of the following (1) to (5), the position being contained in the sequences shown in SEQ ID NOS: 1 to 5, and/or to a complementary sequence thereof, and is used as a primer in the above determination method:

(1) position 10 of the nucleotide sequence of exon 1 of the LT-α gene shown in SEQ ID NO: 1;

(2) position 90 of the nucleotide sequence of intron 1 of the LT-α gene shown in SEQ ID NO: 2;

(3) position ~~81~~ <u>80</u> of the nucleotide sequence of exon 3 of the LT-α gene shown in SEQ ID NO: 3;

(4) position 572 of the nucleotide sequence of the promoter of the IKBL gene shown in SEQ ID NO: 4; and

(5) position 1228 of the nucleotide sequence of the promoter of the BAT1 gene shown in SEQ ID NO: 5.

Page 10, lines 5 - 25

In addition, examples of polymorphisms on the complementary side to be detected in the present invention include gene polymorphisms that exist in at least one complementary sequence selected from the complementary sequence of the lymphotoxin-α (LT-α) gene, that of the I Kappa B-like (IKBL) gene, and that of the BAT1 gene. More specific example is at least one single nucleotide polymorphism selected from the group consisting of the following (1) to (5):

(1) a C/T polymorphism in the complementary sequence of the LT-α gene and at a nucleotide complementary to nucleotide 10 in the nucleotcide sequence of exon 1 of the LT-α gene shown in SEQ ID NO: 1;

(2) a T/C polymorphism in the complementary sequence of the LT-α gene and at a nucleotide complementary to nucleotide 90 in the nucleotide sequence of intron 1 of the LT-α gene shown in SEQ ID NO: 2;

(3) a G/T polymorphism in the complementary sequence of the LT-α gene and at a nucleotide complementary to nucleotide ~~81~~ 80 in the nucleotide sequence of exon 3 of the LT-α gene shown in SEQ ID NO: 3;

(4) an A/T polymorphism in the complementary sequence of the IKBL gene at a nucleotide complementary to nucleotide 572 in the nucleotide sequence of the promoter of the IKBL gene shown in SEQ ID NO: 4; and

(5) a C/G polymorphism in the complementary sequence of the BAT1 gene at a nucleotide complementary to nucleotide 1228 in the nucleotide sequence of the promoter of the BAT1 gene shown in SEQ ID NO: 5.

Page 11, lines 2 - 8

In this specification, nucleotide 90 of the nucleotide sequence of intron 1 of the LT-α gene shown in SEQ ID NO: 2 corresponds to nucleotide 252 (the 252nd nucleotide) from the 1st nucleotide of exon 1 of the LT-α gene. Furthermore, nucleotide ~~81~~ 80 (the ~~81st~~-80th nucleotide) of the nucleotide sequence of exon 3 of the LT-α gene shown in SEQ ID NO: 3 corresponds to nucleotide 723 (the 723rd nucleotide) when counted from the 1st nucleotide of exon 1 of the LT-α gene.

Page 11, lines 9 – 13

Hence, in this specification, the G/A polymorphism at nucleotide 90 of the nucleotide sequence of intron 1 of the LT-α gene shown in SEQ ID NO: 2 may be represented by LT-α intron 1 252G/A, and the C/A polymorphism at nucleotide ~~81~~ 80 of the nucleotide sequence of exon 3 of the LT-α gene shown in SEQ ID NO: 3 may be represented by LT-α exon 3 723C/A.

Page 11, lines 26 – 29; page 12 lines 1 - 7

For example, as shown in the following Table 1, the onset of inflammatory diseases or the existence of a high probability of such onset can be determined when nucleotide 10 of the nucleotide sequence of exon 1 of the LT-α gene shown in SEQ ID NO: 1 is G (LT-α exon 1 10G), when nucleotide 90 of the nucleotide sequence of intron 1 of the LT-α gene shown in SEQ ID NO: 2 is A (LT-α intron 1 252A), when nucleotide ~~81~~ 80 of the nucleotide sequence of exon 3 of the LT-α gene shown in SEQ ID NO: 3 is C (LT-α exon 3 723C), when nucleotide 572 of the nucleotide sequence of the promoter of the IKBL gene shown in SEQ ID NO: 4 is A (IKBL promoter -63A), or when nucleotide 1228 of the nucleotide sequence of the promoter of the BAT1 gene shown in SEQ ID NO: 5 is G (BAT1 promoter -23G).

Page 12, lines 8 – 16

In contrast, a lack of onset of inflammatory diseases or the existence of a low probability of such onset can be determined when nucleotide 10 of the nucleotide sequence of exon 1 of the LT-α gene shown in SEQ ID NO: 1 is A (LT-α exon 1 10A), when nucleotide 90 of the nucleotide sequence of intron 1 of the LT-α gene shown in SEQ ID NO: 2 is G (LT-α intron 1 252G), when nucleotide ~~81~~ 80 of the nucleotide sequence of exon 3 of the LT-α gene shown in SEQ ID NO: 3 is A (LT-α exon 3 723A), when nucleotide 572 of the nucleotide sequence of the promoter of the IKBL gene shown in SEQ ID NO: 4 is T (IKBL promoter -63T), or when nucleotide 1228 of the nucleotide sequence of the promoter of the BAT1 gene shown in SEQ ID NO: 5 is C (BAT1 promoter -23 C).

Page 13, lines 4 – 13

Furthermore, the C/A polymorphism at nucleotide ~~81~~ 80 of the nucleotide sequence of exon 3 of the LT-α gene shown in SEQ ID NO: 3 causes an amino acid mutation from threonine to asparagine because of a change at codon 26 (from ACC to AAC) in exon 3. For example, as shown in the following examples, in the case of codon 26 encoding asparagine (26N), the LT-α expression level is significantly higher than that

in the case where codon 26 encodes threonine (26T), and vascular cell-adhesion molecule-1 (VCAM-1, the cell adhesion factor) and E-selectin are induced in human coronary-artery smooth-muscle cells (HCASMC). Thus, the onset of inflammatory diseases or the existence of a high probability of such onset can be determined.

Page 24, lines 24 – 29; page 25, lines 1 – 25; Part of Example 1

The primers and probes used in this example are as shown below.

(1) LT-α (typing by the invader method)

PCR primer

Forward primer: ACTCAGCCAAGGGTGCAGAG (SEQ ID NO: 9)

Reverse primer: CTTCCTCAGGGATTGAGACCTC (SEQ ID NO: 10)

Probe (SNPs are put in square brackets)

Exon 1 10G>A

TCCAAAGCACGAAGCACGGGCAGCCCAAGGAGATGGGGCAGGAGAGCCTCA CCTGCTGTG[CT]GGAGCCCCTGGGCCCGGACGCTCAGGTCCCTTTATAGAGG AAGCGGCAGTGGCAGCGTGG (SEQ ID NOS: 11 and 12)

Intron 1 90A>G

AGAGAAACCCCAAGGTGAGCAGAGGGAGACAGAGAGAGACAGGAAGGGAA CAGAGAGGAA[TC]CATGGCAGAAACAGAGAATGTGTGACAGAGACAATGAG ACTGACAGATGGAGAGTCAGAG (SEQ ID NOS: 13 and 14)

Exon 3 80~~81~~C>A

TCACACCTTCAGCTGCCCAGACTGCCCGTCAGCACCCCAAGATGCATCTTGCC CACAGCA[CA]CCTCAAACCTGCTGCTCACCTCATTGGTAAACATCCACCTGAC CTCCCAGACATGTCCCC (SEQ ID NOS: 15 and 16)

(2) IKBL (typing by the sequencing method)

PCR primer

Forward primer: TTTAAGGCTCAGGAGCCCAG (SEQ ID NO: 17)

Reverse primer: TCCCTGTTGTTGTCCCACTG (SEQ ID NO: 18)

Sequence primer: ATATCATGTACCCGGCAGAC (SEQ ID NO: 19)

(3) BAT1 (typing by the invader method)

PCR primer

Forward primer: TGGTCTCACATCACTGTTACGC (SEQ ID NO: 20)

Reverse primer: TCTTCCCGCTCGGATTCAG (SEQ ID NO: 21)

Probe:

AAGCTTACCTAAACAGGGAGAGCGCGTATGGCGGCAGCAACAGCGACGAAG GAGGGAAAT[GC]TGCCTTCACTTCCGGTTGCAGGCTTCCCTCTACTCCAGCCT CCCGCCTTCTTGGCTGCAA (SEQ ID NOS: 22 and 23)